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L8: Entry 1 of 1 File: USPT Jun 3, 1997

US-PAT-NO: 5635617
DOCUMENT-IDENTIFIER: US 5635617 A

TITLE: Methods and compositions comprising the agfA gene for detection of Salmonella

DATE-ISSUED: June 3, 1997

INVENTOR-INFORMATION:

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APPL-NO: 8/ 233788 [PALM]
DATE FILED: April 26, 1994

PARENT-CASE:
CROSS-REFERENCE TO RELATED APPLICATIONS This application is a continuation-in-part of U.S. patent application Ser. No. 08/054,452, filed Apr. 26, 1993, abandoned.

INT-CL: [6] C07 H 21/02, C07 H 21/04

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FIELD-OF-SEARCH: 536/23.7, 536/23.2, 536/24.33, 536/23.1

PRIOR-ART-DISCLOSED:

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☐	4689295	August 1987	Taber et al.	435/6
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Tomas and Kay, "Tricarboxylate transport in a Cit.sup.+ Escherichia coli: evidence for the role of an outer membrane protein," Canadian Journal of Microbiology 30: 916-921, 1984.

ART-UNIT: 187
PRIMARY-EXAMINER: Campbell; Eggerton A.
ATTY-AGENT-FIRM: Seed and Berry LLP

ABSTRACT:

An isolated nucleic acid molecule comprising the agfA gene of Salmonella. Methods and compositions suitable for diagnostic tests utilizing the isolated gene, and protein therefrom, to give highly specific diagnostic assays to Salmonella, and/or enteropathogenic bacteria of the family Enterobacteriaceae.

5 Claims, 26 Drawing figures

09/153,596

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=> s immuno(10a)RNA(10a)amplif?
L1           13 IMMUNO(10A) RNA(10A) AMPLIF?

=> dup rem l1
PROCESSING COMPLETED FOR L1
L2            9 DUP REM L1 (4 DUPLICATES REMOVED)

=> d l2 1-9 bib ab

L2   ANSWER 1 OF 9  CAPLUS  COPYRIGHT 2002 ACS
AN   2001:482171  CAPLUS
DN   135:43129
TI   Method of detecting protein by immuno RNA
IN   Eberwine, James; Rodgers, Lori
PA   Trustees of the University of Pennsylvania, USA
SO   U.S., 5 pp., Cont.-in-part of U.S. 5,922,553.
     CODEN: USXXAM
DT   Patent
LA   English
FAN.CNT 2
     PATENT NO.        KIND  DATE           APPLICATION NO.  DATE
     ---------------   ----  --------       ---------------  --------
PI   US 6255060         B1   20010703       US 1999-337944   19990622
     US 5922553         A    19990713       US 1997-972225   19971117
PRAI US 1996-33338      P    19961121
     US 1997-972225     A2   19971117
AB   A method for the detection of a selected protein is provided wherein mRNA
     levels are correlated with the presence of protein using the technique
     referred to herein as immuno-aRNA.
RE.CNT  19    THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD
              ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2   ANSWER 2 OF 9  BIOSIS  COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 1
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AN 2001:301838 BIOSIS
DN PREV200100301838
TI Protein quantification from complex protein mixtures using a proteomics methodology with single-cell resolution.
AU Zhang, Hong-Tao; Kacharmina, Janet E.; Miyashiro, Kevin; Greene, Mark I. (1); Eberwine, James
CS (1) Deparments of Pathology and Laboratory Medicine, Abramson Institute for Cancer Research, University of Pennsylvania, Philadelphia, PA, 19104-6082: greene@reo.med.upenn.edu, eberwine@mscf.med.upenn.edu USA
SO Proceedings of the National Academy of Sciences of the United States of America, (May 8, 2001) Vol. 98, No. 10, pp. 5497-5502. print.
ISSN: 0027-8424.
DT Article
LA English
SL English
AB We have developed an extremely sensitive technique, termed **immuno**-detection **amplified** by T7 **RNA** polymerase (IDAT) that is capable of monitoring proteins, lipids, and metabolites and their modifications at the single-cell level. A double-stranded oligonucleotide containing the T7 promoter is conjugated to an antibody (Ab), and then T7 RNA polymerase is used to amplify RNA from the double-stranded oligonucleotides coupled to the Ab in the Ab-antigen complex. By using this technique, we are able to detect the p185her2/neu receptor from the crude lysate of T6-17 cells at 10-13 dilution, which is 109-fold more sensitive than the conventional ELISA method. Single-chain Fv fragments or complementarity determining region peptides of the Ab also can be substituted for the Ab in IDAT. In a modified protocol, the oligonucleotide has been coupled to an Ab against a common epitope to create a universal detector species. With the linear **amplification** ability of T7 **RNA** polymerase, IDAT represents a significant improvement over **immuno**-PCR in terms of sensitivity and has the potential to provide a robotic platform for proteomics.

L2 ANSWER 3 OF 9 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 2002:4350 BIOSIS
DN PREV200200004350
TI A novel proteomics methodology: **Immuno**-detection **amplified** by T7 **RNA** polymerase.
AU Kacharmina, J. Estee (1); Zhang, H.; Greene, M.; Eberwine, J. (1)
CS (1) Pharmacology, University of Pennsylvania, Philadelphia, PA USA
SO Society for Neuroscience Abstracts, (2001) Vol. 27, No. 2, pp. 2451. print.
Meeting Info.: 31st Annual Meeting of the Society for Neuroscience San Diego, California, USA November 10-15, 2001
ISSN: 0190-5295.
DT Conference
LA English
AB In our continuing efforts to understand the molecular underpinnings of dendritic functioning, we are expanding our studies to include the simultaneous analysis of multiple proteins in neurons. Towards this end we have utilized a novel proteomics methodology termed **immuno**-detection **amplified** by T7 **RNA** polymerase (IDAT) that can quantify the level of multiple proteins in a single cell. This methodology is a modified sandwich ELISA in which Ab-antigen interactions are detected by nucleic acid amplification. A ds-oligo containing a T7 promotor site was covalently coupled to a detector Ab or single-chain Fv fragment and served as the cDNA template. After interaction of the protein target with the detector Ab, RNA amplification was performed. The resulting RNA was labeled with Ribo-Green, and measured with a fluorescent microplate reader. IDAT has recently been used to measure the amount of p185her2/neu, a protein marker for breast cancer, in 3T3 cells and in a single rat hippocampal neuron. We are currently generating phage display peptide libraries enriched for rat hippocampal neuronal or post-synaptic density proteins to be used in conjunction with the IDAT technology. This

proteomics approach will make it possible to screen neurons for the presence and abundance of thousands of proteins and their post-translational modifications in response to neuronal modulation.

L2 ANSWER 4 OF 9 USPATFULL
AN 1999:18920 USPATFULL
TI Method for amplification and detection of RNA and DNA sequences
IN Rossi, John J., Glendora, CA, United States
PA City of Hope, Duarte, CA, United States (U.S. corporation)
PI US 5869249 19990209
AI US 1996-747489 19961112 (8)
RLI Continuation of Ser. No. US 1994-334398, filed on 3 Nov 1994, now patented, Pat. No. US 5622820 which is a continuation of Ser. No. US 1988-180740, filed on 12 Apr 1988, now abandoned which is a continuation-in-part of Ser. No. US 1988-165915, filed on 10 Mar 1988, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Zitomer, Stephanie W.
LREP Rothwell, Figg, Ernst & Kurz
CLMN Number of Claims: 7
ECL Exemplary Claim: 1
DRWN 17 Drawing Figure(s); 13 Drawing Page(s)
LN.CNT 763
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A method of detecting and identifying specific human nucleic acid sequences contained in human nucleic acids in a human blood or tissue sample, comprising: (1) amplifying at least one portion of the specific nucleic acid sequence present in the sample; (2) transcribing the amplification product with an RNA polymerase to produce multiple RNA copies of each copy of specific nucleic acid sequence comprising the amplification product; and (3) identifying the transcription product.

L2 ANSWER 5 OF 9 USPATFULL
AN 1998:150654 USPATFULL
TI Hepatitis C virus epitopes
IN Reyes, Gregory R., Palo Alto, CA, United States
Kim, Jungsuh P., Palo Alto, CA, United States
Moeckli, Randolph, Redwood City, CA, United States
Simonsen, Christian C., Saratoga, CA, United States
PA Genelabs Technologies, Inc., Redwood City, CA, United States (U.S. corporation)
PI US 5843636 19981201
AI US 1995-407410 19950317 (8)
RLI Division of Ser. No. US 1991-681703, filed on 5 Apr 1991, now patented, Pat. No. US 5443965 which is a continuation-in-part of Ser. No. US 1990-594854, filed on 10 Oct 1990, now abandoned which is a continuation-in-part of Ser. No. US 1990-205611, filed on 6 Apr 1990, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Woodward, Michael P.
LREP Dehlinger & Associates
CLMN Number of Claims: 12
ECL Exemplary Claim: 1
DRWN 21 Drawing Figure(s); 21 Drawing Page(s)
LN.CNT 3115
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Peptide antigens which are immunoreactive with sera from individuals infected with hepatitis C virus (HCV) are disclosed. Several of the antigens are immunologically reactive with antibodies present in individuals identified as having chronic and acute HCV infection. The antigens are useful in diagnostic methods for detecting HCV infection in humans. Also disclosed are corresponding genomic-fragment clones

containing polynucleotides encoding the open reading frame sequences for the antigenic peptides.

L2 ANSWER 6 OF 9 MEDLINE
AN 96376777 MEDLINE
DN 96376777 PubMed ID: 8782649
TI Detection of N-acetylgalactosaminyltransferase mRNA which determines expression of Sda blood group carbohydrate structure in human gastrointestinal mucosa and cancer.
AU Dohi T; Yuyama Y; Natori Y; Smith P L; Lowe J B; Oshima M
CS Biochemistry and Nutrition Division, Research Institute, International Medical Center of Japan, Tokyo.
SO INTERNATIONAL JOURNAL OF CANCER, (1996 Sep 4) 67 (5) 626-31.
Journal code: GQU; 0042124. ISSN: 0020-7136.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-S83275
EM 199610
ED Entered STN: 19961106
Last Updated on STN: 19980206
Entered Medline: 19961024
AB The Sda blood group carbohydrate structure, GalNAcbeta1-4[NeuAcalpha2-3]Galbeta1-4GlcNAc-R, is expressed on glycolipid and glycoprotein in human gastrointestinal mucosa. The expression of the Sda determinant dramatically decreases in cancer tissue. The activity of the beta1,4N-acetylgalactosaminyltransferase (Sda-GalNAcT), which transfers GalNAc to NeuAcalpha2-3Galbeta1-4Glc(NAc)-R, correlates with the expression of the Sda **immuno**-epitope. From the total **RNA** fraction of human gastric mucosa, we have **amplified** a cDNA segment by reverse-transcription-polymerase-chain reaction (RT-PCR), using primers designed according to the cDNA sequence of a murine beta1,4GalNAcT which synthesizes the Sda determinant. An RT-PCR product of 390 bp shared 85% nucleotide identity with the murine Sda-related beta1,4GalNAcT. This RT-PCR product hybridized to a transcript in mRNA prepared from human gastric mucosa. In RT-PCR using specific primers to this PCR product, Sda-GalNAcT mRNA was detected in all samples of normal stomach and small intestine examined and the majority of normal colonic specimens. Six out of nine cases of gastric cancer, and 9 out of 13 cases of colonic cancer failed to produce the target DNA. These results correlate with the beta1,4GalNAcT activity measured in the same samples. In conclusion, a segment of the cDNA for beta1,4GalNAcT which determines expression of the Sda carbohydrate structure was obtained, and reduced transcription of this beta 1,4GalNAcT resulted in the disappearance of the Sda epitope in gastrointestinal cancer.

L2 ANSWER 7 OF 9 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 2
AN 1992:326726 BIOSIS
DN BA94:28567
TI ISOLATION AND AMPLIFICATION OF HUMAN IGE FD ENCODING MRNA FROM HUMAN PERIPHERAL BLOOD LYMPHOCYTES.
AU WALKER M R; BEVAN L J; DANIELS J; ROTTIER M M A; RAPLEY R; ROBERTS A M
CS MOLECULAR BIOLOGY RES. GROUP, UNIVERSITY DEP. CLINICAL BIOCHEIMSTRY, WOLFSON RES. LAB., QUEEN ELIZABETH MEDICAL CENTRE, EDGBASTON, BIRMINGHAM B15 2TH, UK.
SO J IMMUNOL METHODS, (1992) 149 (1), 77-85.
CODEN: JIMMBG. ISSN: 0022-1759.
FS BA; OLD
LA English
AB In order to establish the feasibility of applying recombinatorial library technologies to investigate human in vivo IgE responses, and as a pre-requisite of recombinatorial library construction, we have attempted to determine workable peripheral blood sample volumes required for

isolation of mRNA for polymerase chain raction (PCR) amplification of human IgE Fd encoding sequences. Cells secreting chimeric human IgE monoclonal antibody specific for the hapten NIP were used to establish the conditions for specific amplification of C.epsilon.1 domain and Fd encoding sequences, as determined by Southern hybridisation. Amplification of C.epsilon.1 domain sequences could be achieved using as few as ten cultured cells as the source of RNA. Specific IgE+ B cell enrichment using **immuno**-magnetic particles prior to **RNA** extraction was, however, required to obtain **amplification** of IgE C.epsilon.1 and Fd fragments from lymphocytes prepared from 40 ml human peripheral blood. IgG1+ B cell enrichment from similar samples was not required for detectable amplification of human C.gamma.1 cDNA sequences. However, this procedure improved amplification efficiency. Optimisation of methods to separate specific B cell populations, or specific RNA/cDNA sequences, will facilitate in vitro generation of human IgE Fab fragments from peripheral blood.

L2 ANSWER 8 OF 9 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1983:291438 BIOSIS
DN BA76:48930
TI CONSTRUCTION OF A MODULAR DI HYDRO FOLATE REDUCTASE COMPLEMENTARY DNA GENE ANALYSIS OF SIGNALS UTILIZED FOR EFFICIENT EXPRESSION.
AU KAUFMAN R J; SHARP P A
CS DEP. BIOL., MASS. INST. TECHNOL., CAMBRIDGE, MASS. 02139.
SO MOL CELL BIOL, (1982) 2 (11), 1304-1319.
CODEN: MCEBD4. ISSN: 0270-7306.
FS BA; OLD
LA English
AB Dihydrofolate reductase (DHFR) modular genes were constructed with segments containing the adenovirus major late promoter, a 3' splice site from a variable region Ig gene, a DHFR c[complementary]DNA, and portions of the SV40 genome. DNA-mediated transfer of these genes transformed Chinese hamster ovary [CHO] DHFR- cells to the DHFR+ phenotype. Transformants contained one to several copies of the transfected DNA integrated into the host genome. Clones subjected to growth in increasing concentrations of methotrexate eventually gave rise to lines containing several hundred copies of the transforming DNA. Analysis of the DHFR mRNA produced in amplified lines indicated the following. All clones utilize the adenovirus major late promoter for transcription initiation. A hybrid intron formed by the 5' splice site of the adenovirus major late leader and a 3' splice site from a variable-region Ig gene is properly excised. The mRNA is not efficiently polyadenylated at sequences in the 3' end of the DHFR cDNA but rather uses polyadenylation signals downstream from the DHFR cDNA. Three independent clones produce a DHFR mRNA containing SV40 or pBR322 and SV40 sequences, and the RNA is polyadenylated at the SV40 late polyadenylation site. Another clone has recombined into cellular DNA and apparently uses a cellular sequence for polyadenylation. Introduction of a segment containing the SV40 early polyadenylation signal into the 3' end of the DHFR cDNA gene generated a recombinant capable of transforming cells to the DHFR+ phenotype with at least a 10-fold increase in efficiency, demonstrating the necessity for an efficient polyadenylation signal. Attachment of a DNA segment containing the transcription enhancer (72-base pair repeat) of SV40 further increased the biological activity of the modular DHFR gene 50- to 100-fold.

L2 ANSWER 9 OF 9 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1981:176634 BIOSIS
DN BA71:46626
TI A HIGH PRODUCTION RATE OF TRANSLATABLE **IMMUNO** GLOBULIN G MESSENGER **RNA** ACCOUNTS FOR THE **AMPLIFIED** SYNTHESIS OF **IMMUNO** GLOBULIN G IN MYELOMA CELLS.
AU WALLACH M; LASKOV R
CS THE HUBERT H. HUMPHREY CENTER FOR EXPERIMENTAL MEDICINE AND CANCER RESEARCH, THE HEBREW UNIVERSITY-HADASSAH MEDICAL SCHOOL, JERUSALEM,

ISRAEL.

SO EUR J BIOCHEM, (1980) 110 (2), 545-554.
CODEN: EJBCAI. ISSN: 0014-2956.
FS BA; OLD
LA English

AB The accumulation of Ig mRNA in myeloma cells was studied. Specific mRNA for L and H chains of IgG were isolated from the murine MPC-11 myeloma tumor cells by immune precipitation of polysomes which synthesize these chains. The immune-precipitated polysomes were enriched 10- to 30-fold in the .gamma. and .vkappa. mRNA sequences, respectively. In the wheat germ cell-free system the .vkappa. mRNA preparation was translated mainly into 3 polypeptides of MW 25,000, 18,000 and 15,000. Immune precipitation of polysomes was also used to characterize 3 variant clones of MPC-11 myeloma. Little if any .gamma.-chain polysomes are present in the L-chain producer and non-producer clones, while a substantial amount of .vkappa.-chain polysomes was present in the non-producer clone. This may be due to the presence in the non-producer cells of the constant region .vkappa.-chain fragment. In order to determine the relative synthesis rate of .vkappa. and .gamma. mRNA, pulse-labeled polysomes were immune precipitated using antibodies to .vkappa. and .gamma. chains. .vkappa. and .gamma. mRNA molecules are produced at a very high relative rate each accounting for 10-15% of the total labeled mRNA after 1 h of labeling. These values are higher than the steady-state pool size of .vkappa. and .gamma. mRNA, which was 5-6%, and indicates that the half-life of these molecules is not unusually high. The amplified synthesis of Ig chains in myeloma cells is mainly due to a high rate of production of translatable .vkappa. and .gamma. mRNA.

=>

L2 ANSWER 4 OF 9 USPATFULL

SUMM **Amplification** of an **RNA** template is particularly advantageous for detecting retroviruses, such as human **immuno** -deficiency virus (HIV or human T-lymphotropic virus HTLV III/LAV). HIV has been shown to be the etiological agent of acquired immune. . .

L2 ANSWER 5 OF 9 USPATFULL

DETD . . . as 409-1-1(c-a), do yield HCV-specific immunopositive signals with selected samples. Accordingly, the two methods presented in the present invention, (i) **immuno**-screening of cDNA libraries generated directly from sera-derived **RNA**, and (ii) immunoscreening of **amplified**-fragment libraries, can both be seen to be effective methods of identifying cDNA sequences encoding viral antigens. Further, confirmation of the. . .